

RAW SEQUENCE LISTING

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Application Serial Number: 09/721,114A
Source: FW 16
Date Processed by STIC: 1-6-05

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IFW16

RAW SEQUENCE LISTING

DATE: 01/06/2005

PATENT APPLICATION: US/09/721,114A

TIME: 16:23:35

Input Set : A:\MAFF1.txt

Output Set: N:\CRF4\01062005\I721114A.raw

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3 <110> APPLICANT: Hirohiko Hirochika
4     Muneo Yamazaki
5     Akio Miyao
7 <120> TITLE OF INVENTION: A novel gene involved in brassinosteroid responses
9 <130> FILE REFERENCE: MAFF-1
11 <140> CURRENT APPLICATION NUMBER: US 09/721,114A
12 <141> CURRENT FILING DATE: 2000-11-22
14 <150> PRIOR APPLICATION NUMBER: JP 2000-149106
15 <151> PRIOR FILING DATE: 2000-05-19
17 <160> NUMBER OF SEQ ID NOS: 5
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 4310
23 <212> TYPE: DNA
24 <213> ORGANISM: Oryza sativa
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (655)..(3828)
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35 ctcgatacga atccaccgcg gcgcgcccgc gcgcctgcgt cctcttccct ccccgggagc 180
37 cgaccgacca cgccgaccag tcgatctccc tctccgggcg ccaaccgcgt cttagcttca 240
39 tcgaatccac cgccccaccc cgcactctct cctcctcctc cgacgacgac gactactact 300
41 agtctttctcc aataagcccc cctcccgcgc cccccgcctg aagaagaagc agcagctagc 360
43 tccgggggaga ggtagcagcg gcgcggggta gatcgcgccc cgccccgcct gcgtcgcggc 420
45 tgtcggagca aacgcaaacc cccaggttg ttctagcgtg tgcagcggct agctgattga 480
47 ttgtcttctg tgatatatcc agagctcgtg ttttgtggtt tgtggtttgt ggtttgtgct 540
49 tggattgttg atgtgcta atcgcgcggtt acaagatcac tgctggattg atattgagtt 600
51 gtgcctcggc tgtgctagct gtgtgttgat tctctcctcg tcgtggtgat cgat atg 657
52                                     Met
53                                     1
55 gag att gtt gca gta gat cag gag gga gct cgt gtt gtt ggg acg aac 705
56 Glu Ile Val Ala Val Asp Gln Glu Gly Ala Arg Val Val Gly Thr Asn
57           5           10           15
59 tgt atg ctt gct cgt ggt gga act ggt gct gta gcg cca gtg ttg gag 753
60 Cys Met Leu Ala Arg Gly Gly Thr Gly Ala Val Ala Pro Val Leu Glu
61           20           25           30
63 ctg aca gcg acg cct cgt cag gat gca gcc gct gaa gct ggt gta gac 801
64 Leu Thr Ala Thr Pro Arg Gln Asp Ala Ala Ala Glu Ala Gly Val Asp
65           35           40           45
67 gaa ccg gca caa cac caa tgc gag cat ttc tcc ata aga ggg tat gtt 849
68 Glu Pro Ala Gln His Gln Cys Glu His Phe Ser Ile Arg Gly Tyr Val

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69	50				55				60				65				
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72	Ala	Leu	Leu	Gln	Lys	Lys	Asp	Pro	Lys	Phe	Cys	Ser	Leu	Ser	Arg	Ile	
73					70				75				80				
75	ttc	cat	gac	cag	aaa	aaa	tgt	gat	gaa	cac	aaa	gct	agt	tca	agc	cca	945
76	Phe	His	Asp	Gln	Lys	Lys	Cys	Asp	Glu	His	Lys	Ala	Ser	Ser	Ser	Pro	
77					85				90				95				
79	ttt	tct	gta	gca	aag	ttt	cga	cga	tgg	gat	tgc	tcg	aag	tgc	ttg	gat	993
80	Phe	Ser	Val	Ala	Lys	Phe	Arg	Arg	Trp	Asp	Cys	Ser	Lys	Cys	Leu	Asp	
81				100				105					110				
83	aag	ttg	aaa	act	tca	gat	aat	gga	aca	gca	cca	aga	act	ctt	ccc	gca	1041
84	Lys	Leu	Lys	Thr	Ser	Asp	Asn	Gly	Thr	Ala	Pro	Arg	Thr	Leu	Pro	Ala	
85		115					120					125					
87	aag	cag	aat	ggc	aca	agt	gat	ggt	tgc	tcc	atc	aca	ttt	gtt	cgg	agc	1089
88	Lys	Gln	Asn	Gly	Thr	Ser	Asp	Gly	Cys	Ser	Ile	Thr	Phe	Val	Arg	Ser	
89	130						135				140				145		
91	act	ttt	gtg	cct	gct	agt	gtt	ggt	tcc	caa	aaa	gtg	tct	cct	agc	aca	1137
92	Thr	Phe	Val	Pro	Ala	Ser	Val	Gly	Ser	Gln	Lys	Val	Ser	Pro	Ser	Thr	
93					150				155					160			
95	caa	tca	tct	caa	ggg	aag	aat	gct	gat	aga	tca	act	ctt	cca	aag	agt	1185
96	Gln	Ser	Ser	Gln	Gly	Lys	Asn	Ala	Asp	Arg	Ser	Thr	Leu	Pro	Lys	Ser	
97				165				170					175				
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101			180					185					190				
103	gga	gct	gct	gag	gcc	aat	act	gat	tca	cca	atg	aaa	gat	ttg	caa	ggg	1281
104	Gly	Ala	Ala	Glu	Ala	Asn	Thr	Asp	Ser	Pro	Met	Lys	Asp	Leu	Gln	Gly	
105		195					200					205					
107	cca	gcc	caa	aat	tat	gat	gtg	gca	gca	aat	gtc	tct	gag	gac	aac	act	1329
108	Pro	Ala	Gln	Asn	Tyr	Asp	Val	Ala	Ala	Asn	Val	Ser	Glu	Asp	Asn	Thr	
109	210					215					220				225		
111	tct	gtt	gat	gtt	ggg	gct	tta	cct	gaa	gtt	ccc	cag	att	aca	tgg	cac	1377
112	Ser	Val	Asp	Val	Gly	Ala	Leu	Pro	Glu	Val	Pro	Gln	Ile	Thr	Trp	His	
113					230				235					240			
115	ata	gaa	gta	aat	ggt	gca	gat	caa	cct	cca	tcc	act	cca	aaa	ctt	tct	1425
116	Ile	Glu	Val	Asn	Gly	Ala	Asp	Gln	Pro	Pro	Ser	Thr	Pro	Lys	Leu	Ser	
117				245				250					255				
119	gaa	gtg	gtc	ctc	aaa	aga	aat	gaa	gat	gaa	aat	gga	aaa	act	gaa	gag	1473
120	Glu	Val	Val	Leu	Lys	Arg	Asn	Glu	Asp	Glu	Asn	Gly	Lys	Thr	Glu	Glu	
121			260					265					270				
123	act	ctt	gtt	gct	gag	cag	tgc	aat	ttg	acc	aaa	gat	cct	aac	cca	atg	1521
124	Thr	Leu	Val	Ala	Glu	Gln	Cys	Asn	Leu	Thr	Lys	Asp	Pro	Asn	Pro	Met	
125		275				280						285					
127	tct	gga	aag	gaa	cgt	gat	cag	gtt	gct	gag	cag	tgc	aat	ttg	acc	aaa	1569
128	Ser	Gly	Lys	Glu	Arg	Asp	Gln	Val	Ala	Glu	Gln	Cys	Asn	Leu	Thr	Lys	
129	290					295				300				305			
131	gat	ccg	aaa	cca	gtg	tct	ggg	cag	aaa	tgt	gag	cag	atc	tgc	aat	gag	1617
132	Asp	Pro	Lys	Pro	Val	Ser	Gly	Gln	Lys	Cys	Glu	Gln	Ile	Cys	Asn	Glu	
133					310				315					320			

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135 cca tgt gaa gaa gtt gtt ctc aaa aga agc tcc aaa tct aag agg aag 1665
136 Pro Cys Glu Glu Val Val Leu Lys Arg Ser Ser Lys Ser Lys Arg Lys
137          325          330          335
139 acg gat aag aag ttg atg aag aag cag cag cac agc aag aaa cgc act 1713
140 Thr Asp Lys Lys Leu Met Lys Lys Gln Gln His Ser Lys Lys Arg Thr
141          340          345          350
143 gcc cag gct gat gtt tca gat gca aag ctt tgt cgg aga aag cca aaa 1761
144 Ala Gln Ala Asp Val Ser Asp Ala Lys Leu Cys Arg Arg Lys Pro Lys
145          355          360          365
147 aag gtg cgg ctt cta tca gaa att ata aat gct aac cag gtt gag gat 1809
148 Lys Val Arg Leu Leu Ser Glu Ile Ile Asn Ala Asn Gln Val Glu Asp
149 370          375          380          385
151 tct aga agt gac gaa gtt cat cgt gaa aat gcc gct gat ccc tgt gag 1857
152 Ser Arg Ser Asp Glu Val His Arg Glu Asn Ala Ala Asp Pro Cys Glu
153          390          395          400
155 gat gat aga agt acc atc ccg gtc ccg atg gaa gta agc atg gat att 1905
156 Asp Asp Arg Ser Thr Ile Pro Val Pro Met Glu Val Ser Met Asp Ile
157          405          410          415
159 cct gtt agc aac cat aca gtg gga gaa gat ggg tta aaa tca agt aag 1953
160 Pro Val Ser Asn His Thr Val Gly Glu Asp Gly Leu Lys Ser Ser Lys
161          420          425          430
163 aac aag aca aaa cgc aaa tac tct gat gtt gta gat gat gga tca tca 2001
164 Asn Lys Thr Lys Arg Lys Tyr Ser Asp Val Val Asp Asp Gly Ser Ser
165          435          440          445
167 ctt atg aac tgg ctg aat gga aaa aag aaa aga act gga agt gtg cat 2049
168 Leu Met Asn Trp Leu Asn Gly Lys Lys Lys Arg Thr Gly Ser Val His
169 450          455          460          465
171 cac aca gtt gct cat cca gct ggg aat ttg agc aac aaa aaa gtg aca 2097
172 His Thr Val Ala His Pro Ala Gly Asn Leu Ser Asn Lys Lys Val Thr
173          470          475          480
175 ccc act gcg agt act cag cat gat gat gag aat gat act gaa aat ggt 2145
176 Pro Thr Ala Ser Thr Gln His Asp Asp Glu Asn Asp Thr Glu Asn Gly
177          485          490          495
179 ctt gac aca aat atg cat aag aca gat gtc tgt cag cat gta tca gaa 2193
180 Leu Asp Thr Asn Met His Lys Thr Asp Val Cys Gln His Val Ser Glu
181          500          505          510
183 atc tcc aca cag agg tgc tca tca aag ggg aaa aca gcg ggt ttg agt 2241
184 Ile Ser Thr Gln Arg Cys Ser Ser Lys Gly Lys Thr Ala Gly Leu Ser
185          515          520          525
187 aag ggg aaa aca cat tca gct gct agt acc aaa tat ggt ggt gaa agc 2289
188 Lys Gly Lys Thr His Ser Ala Ala Ser Thr Lys Tyr Gly Gly Glu Ser
189 530          535          540          545
191 acc aga aat ggt cag aac ata cat gta ctc agc gca gaa gat caa tgc 2337
192 Thr Arg Asn Gly Gln Asn Ile His Val Leu Ser Ala Glu Asp Gln Cys
193          550          555          560
195 cag atg gaa acc gaa aac tct gtt ctg agt cac tcg gca aag gtt tct 2385
196 Gln Met Glu Thr Glu Asn Ser Val Leu Ser His Ser Ala Lys Val Ser
197          565          570          575
199 cca gct gag cat gat atc caa att atg tct gac ctt cat gag cag agt 2433

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200 Pro Ala Glu His Asp Ile Gln Ile Met Ser Asp Leu His Glu Gln Ser
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203 cta ccc aag aag aaa aag aag caa aaa ctt gaa gtg act cgt gaa aaa 2481
204 Leu Pro Lys Lys Lys Lys Lys Gln Lys Leu Glu Val Thr Arg Glu Lys
205      595      600      605
207 cag acc atg ata gat gac atc ccc atg gat att gtt gaa ctg cta gct 2529
208 Gln Thr Met Ile Asp Asp Ile Pro Met Asp Ile Val Glu Leu Leu Ala
209 610      615      620      625
211 aaa aac cag cat gag agg cag ctt atg act gag act gat tgt tct gac 2577
212 Lys Asn Gln His Glu Arg Gln Leu Met Thr Glu Thr Asp Cys Ser Asp
213      630      635      640
215 atc aac cgt att caa tcc aag aca act gct gat gat gat tgt gta ata 2625
216 Ile Asn Arg Ile Gln Ser Lys Thr Thr Ala Asp Asp Asp Cys Val Ile
217      645      650      655
219 gta gct gcc aag gat ggt tca gat tat gca tca agt gtg ttt gac act 2673
220 Val Ala Ala Lys Asp Gly Ser Asp Tyr Ala Ser Ser Val Phe Asp Thr
221      660      665      670
223 aat tcc caa cag aag tcc ttg gca tcc caa agt aca cag aag gag tta 2721
224 Asn Ser Gln Gln Lys Ser Leu Ala Ser Gln Ser Thr Gln Lys Glu Leu
225      675      680      685
227 cag ggt cat ttg gca ttg acc aca caa gag tct cca cat cct cag aac 2769
228 Gln Gly His Leu Ala Leu Thr Thr Gln Glu Ser Pro His Pro Gln Asn
229 690      695      700      705
231 ttt cag tct act cag gaa cag cag aca cat ttg cgg atg gaa gaa atg 2817
232 Phe Gln Ser Thr Gln Glu Gln Gln Thr His Leu Arg Met Glu Glu Met
233      710      715      720
235 gtc act att gct gca agc tca cca cta ttt tca cat cat gat gat cag 2865
236 Val Thr Ile Ala Ala Ser Ser Pro Leu Phe Ser His His Asp Asp Gln
237      725      730      735
239 tat att gct gaa gca cca act gaa cat tgg ggc cgt aag gac gca aag 2913
240 Tyr Ile Ala Glu Ala Pro Thr Glu His Trp Gly Arg Lys Asp Ala Lys
241      740      745      750
243 aag cta acg tgg gag caa ttt aag gcc act aca aga aat tct cca gca 2961
244 Lys Leu Thr Trp Glu Gln Phe Lys Ala Thr Thr Arg Asn Ser Pro Ala
245      755      760      765
247 gca aca tgt ggt gct caa ttt aga cct ggt atc caa gca gtt gac ttg 3009
248 Ala Thr Cys Gly Ala Gln Phe Arg Pro Gly Ile Gln Ala Val Asp Leu
249 770      775      780      785
251 act tct act cat gtc atg gga tct tcc agc aat tat gca tct cgc caa 3057
252 Thr Ser Thr His Val Met Gly Ser Ser Ser Asn Tyr Ala Ser Arg Gln
253      790      795      800
255 cca gta att gcg cca ctg gac cgc tat gct gaa aga gcg gtt aac cag 3105
256 Pro Val Ile Ala Pro Leu Asp Arg Tyr Ala Glu Arg Ala Val Asn Gln
257      805      810      815
259 gtc cat gca aga aat ttt cca agc aca ata gca acc atg gaa gcg agt 3153
260 Val His Ala Arg Asn Phe Pro Ser Thr Ile Ala Thr Met Glu Ala Ser
261      820      825      830
263 aag tta tgt gat cgg aga aat gct gga caa gta gtc ttg tat cct aaa 3201
264 Lys Leu Cys Asp Arg Arg Asn Ala Gly Gln Val Val Leu Tyr Pro Lys

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267	gaa tcc atg cct gcg acg cat ctt ctg aga atg atg gat cca tca aca	3249		
268	Glu Ser Met Pro Ala Thr His Leu Leu Arg Met Met Asp Pro Ser Thr			
269	850	855	860	865
271	tta gca agc ttc ccc aac tat gga act tct agc agg aac cag atg gag	3297		
272	Leu Ala Ser Phe Pro Asn Tyr Gly Thr Ser Ser Arg Asn Gln Met Glu			
273		870	875	880
275	tct caa ctt cat aat tct cag tat gca cat aat cag tac aaa gga tca	3345		
276	Ser Gln Leu His Asn Ser Gln Tyr Ala His Asn Gln Tyr Lys Gly Ser			
277		885	890	895
279	acc agc aca tca tat ggc agt aac ctg aat gga aag att cca ttg aca	3393		
280	Thr Ser Thr Ser Tyr Gly Ser Asn Leu Asn Gly Lys Ile Pro Leu Thr			
281		900	905	910
283	ttc gaa gac tta tca cgg cat cag ctg cat gat ctg cac aga cct tta	3441		
284	Phe Glu Asp Leu Ser Arg His Gln Leu His Asp Leu His Arg Pro Leu			
285		915	920	925
287	cgc cca cat cct aga gtt ggt gtg ctt ggc tcc ttg ctg cag aag gaa	3489		
288	Arg Pro His Pro Arg Val Gly Val Leu Gly Ser Leu Leu Gln Lys Glu			
289	930	935	940	945
291	att gca aac tgg tgc gag aac tgt ggc aca caa tct ggt tat aag tta	3537		
292	Ile Ala Asn Trp Ser Glu Asn Cys Gly Thr Gln Ser Gly Tyr Lys Leu			
293		950	955	960
295	gga gtg tca aca gga ata aca tgc cat cag atg aac aga aag gaa cat	3585		
296	Gly Val Ser Thr Gly Ile Thr Ser His Gln Met Asn Arg Lys Glu His			
297		965	970	975
299	ttt gaa gcc ctg aat tct gga atg ttt tca gca aaa tgg aat gca ttg	3633		
300	Phe Glu Ala Leu Asn Ser Gly Met Phe Ser Ala Lys Trp Asn Ala Leu			
301		980	985	990
303	cag ttg ggt tct gtt agc tcc agt gca gat ttt tta tca gcg agg aac	3681		
304	Gln Leu Gly Ser Val Ser Ser Ser Ala Asp Phe Leu Ser Ala Arg Asn			
305		995	1000	1005
307	agc ata gct caa tct tgg acc aga ggc aag ggt aaa atg gtt cat ccc	3729		
308	Ser Ile Ala Gln Ser Trp Thr Arg Gly Lys Gly Lys Met Val His Pro			
309	1010	1015	1020	1025
311	ttg gat cgg ttt gtg aga cag gat atc tgt ata act aac aag aac cca	3777		
312	Leu Asp Arg Phe Val Arg Gln Asp Ile Cys Ile Thr Asn Lys Asn Pro			
313		1030	1035	1040
315	gct gat ttt act aca atc agt aac gat aac gag tat atg gat tac cgc	3825		
316	Ala Asp Phe Thr Thr Ile Ser Asn Asp Asn Glu Tyr Met Asp Tyr Arg			
317		1045	1050	1055
319	tga agcagaaagt ggtgtgcata attcctgaac atttacaatc atacatttca	3878		
322	tctttatggc gccaaatagt catactgtaa gaggagggt ttgctggatc tgctgtaagg	3938		
324	cttcttgtaa gttgtggatg cccattttc tggatgggaa cctgccagac agtgaacaag	3998		
326	ggctttgcaa ggtgcagcat ccggtttttg ttttgccagt ccaagaaacg tctcctgtt	4058		
328	actttgtagt tgtactcata ctagtgcgt tgtttgtaca aggagaaatg tgtaaccttg	4118		
330	ttgaaaaaat gtctccccca ttttgaatt accataagga ggtttatagt gttgtgagct	4178		
332	gtgtgtgact gacggcgaga aatggttttg tcggtgttaa gggtgaaacg actagctctc	4238		
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